Untitled

itle: US-10-536-935A-1
Perfect score: 1497
Sequence: 1 atggcaacagtacatcagaa..........gaatattcattaagctataa 1497

title: US-10-536-935A-1
Perfect score: 1497
Sequence: 1 atggcaacagtacatcagaa..........gaatattcattaagctataa 1497

RESULT 1
ABL88606
ID   ABL88606 standard; DNA; 1497 BP.
XX
AC   ABL88606;
XX
DT   20-MAY-2002 (first entry)
XX
DE   Fungal cell wall synthesis related polynucleotide SEQ ID NO 1.
XX
KW   Fungi; transport; GPI anchor protein; cell wall; biosynthesis; fungicide;
KW   antifungal; 1-(4-n-butylbenzyl)isoquinoline; gene; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200204626-A1.
XX
PD   17-JAN-2002.
XX
PF   06-JUL-2001; 2001WO-JP005899.
XX
PR   07-JUL-2000; 2000JP-00206968.
PR   17-OCT-2000; 2000JP-00316027.
XX
PA   (EISA) EISAI CO LTD.
XX
PI   Tsukahara K, Hata K, Sagane K, Nakamoto K, Tsuchiya M,
PI   Watanabe N, Oba F, Tsukada I, Ueda N, Tanaka K, Kai J;
XX
DR   WPI; 2002-241441/29.
DR   P-PSDB; ABB88538.
XX
PT   Fungal cell wall synthesis gene encoding protein related to transport
PT   process of GPI anchor protein to cell wall, useful in screening
PT   inhibitors for development into antifungal agents.
XX
PS   Claim 1; Page 213-216; 297pp; Japanese.
XX
CC   The invention relates to a DNA overexpressed in fungi that encodes a
CC   protein imparting tolerance to compounds that inhibit the transport
CC   process of the GPI anchor protein to the cell wall in fungi. The
CC   inhibitors have fungicide activity through inhibition of fungal cell wall
CC   synthesis. The gene and encoded protein are useful in screening for
CC   inhibitors for development into antifungal agents, particularly for
CC   patients with opportunistic fungal infection. A gene imparting tolerance
CC   to e.g. 1-(4-n-butylbenzyl)isoquinoline can be identified. Such
CC   antifungals are likely to be more effective because of its novel
CC   mechanism of action. The present sequence is that of a polynucleotide of
CC   the invention
XX
SQ   Sequence 1497 BP; 429 A; 269 C; 275 G; 524 T; 0 U; 0 Other;

Query Match   100.0%; Score 1497; DB 6; Length 1497;
Best Local Similarity   100.0% Pred. No. 0;
Matches 1497; Conservative   0; Msmatches   0; Indels   0; Gaps   0;

```
Qy        1 ATGGCAACAGTACATCAGAAGAATATGTCGACTTTAAAACAGAGAAAAGAGGACTTTGTG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGCAACAGTACATCAGAAGAATATGTCGACTTTAAAACAGAGAAAAGAGGACTTTGTG 60

Qy       61 ACAGGGCTCAATGGCCGGTTCTATAACAGAAATTAACGCAGTGACATCAATTGCTTTGGTA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ACAGGGCTCAATGGCCGGTTCTATAACAGAAATTAACGCAGTGACATCAATTGCTTTGGTA 120

Qy      121 ACTTACATATCATGGAACTTATTGAAAAATTCCAACCTTATGCCTCCTGGCATTTCCAGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACTTACATATCATGGAACTTATTGAAAAATTCCAACCTTATGCCTCCTGGCATTTCCAGC 180

Qy      181 GTGCAATACATAATTGATTTTGCATTGAACTGGGTTGCTTTGCTTCTATCTATTACTATT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GTGCAATACATAATTGATTTTGCATTGAACTGGGTTGCTTTGCTTCTATCTATTACTATT 240

Qy      241 TATGCTAGTGAACCATACCTTCTAAACACGCTAATACTGTTACCTTGTTTGCTCGCATTC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TATGCTAGTGAACCATACCTTCTAAACACGCTAATACTGTTACCTTGTTTGCTCGCATTC 300

Qy      301 ATATATGGAAAATTTACTAGCTCGAGTAAACCTTCTAATCCAATATACAATAAAAAAAAA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ATATATGGAAAATTTACTAGCTCGAGTAAACCTTCTAATCCAATATACAATAAAAAAAAA 360

Qy      361 ATGATTACACAGCCGGTTCCAACTAGAAAAAAAGCCGTATATTACTGCGTATCGTGGTGGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ATGATTACACAGCCGGTTCCAACTAGAAAAAAAGCCGTATATTACTGCGTATCGTGGTGGG 420

Qy      421 ATGCTTATTCTGACTGCTATTGCCATCTTGGCTGTAGATTTTCCAATTTTCCCAAGGAGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 ATGCTTATTCTGACTGCTATTGCCATCTTGGCTGTAGATTTTCCAATTTTCCCAAGGAGG 480

Qy      481 TTTGCCAAGGTGGAAACTTGGGGGACATCCCTGATGGATCTTGGTGTAGGATCATTCGTT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TTTGCCAAGGTGGAAACTTGGGGGACATCCCTGATGGATCTTGGTGTAGGATCATTCGTT 540

Qy      541 TTCAGTAACGGTATTGTTTCTTCTAGGGCACTGTTGAAAAACCTAAGCTTGAAGAGTAAA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TTCAGTAACGGTATTGTTTCTTCTAGGGCACTGTTGAAAAACCTAAGCTTGAAGAGTAAA 600

Qy      601 CCCAGCTTCTTAAAAAATGCATTTAATGCCTTAAAATCAGGAGGAACTCTATTGTTCCTA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CCCAGCTTCTTAAAAAATGCATTTAATGCCTTAAAATCAGGAGGAACTCTATTGTTCCTA 660

Qy      661 GGATTGCTGAGGTTGTTTTTTTGTAAAAAATTTGGAATATCAAGAACATGTCACAGAATAT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GGATTGCTGAGGTTGTTTTTTTGTAAAAAATTTGGAATATCAAGAACATGTCACAGAATAT 720

Qy      721 GGGGTTCATTGGAATTTTTTTTATCACCCTATCATTGTTGCCACTTGTATTGACCTTTATT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GGGGTTCATTGGAATTTTTTTTATCACCCTATCATTGTTGCCACTTGTATTGACCTTTATT 780

Qy      781 GATCCCGTCACAAGAATGGTTCCACGCTGCTCAATTGCAATATTCATTTCATGCATTTAT 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GATCCCGTCACAAGAATGGTTCCACGCTGCTCAATTGCAATATTCATTTCATGCATTTAT 840

Qy      841 GAATGGCTACTTTTAAAGGACGATCGCACTTTAAACTTTTTAATTTTGGCTGATAGAAAT 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    841 GAATGGCTACTTTTAAAGGACGATCGCACTTTAAACTTTTTAATTTTGGCTGATAGAAAT 900

Qy    901 TGTTTCTTCAGTGCTAATAGAGAAGGCATCTTCTCATTTCTAGGTTATTGCTCGATTTTT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGTTTCTTCAGTGCTAATAGAGAAGGCATCTTCTCATTTCTAGGTTATTGCTCGATTTTT 960

Qy    961 CTTTGGGGCCAAAACACGGGATTTTACTTGTTGGGAAATAAACCAACTTTAAACAATCTT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTTTGGGGCCAAAACACGGGATTTTACTTGTTGGGAAATAAACCAACTTTAAACAATCTT 1020

Qy   1021 TATAAGCCTTCTACGCAAGACGTAGTTGCAGCATCAAAGAAGTCTTCGACTTGGGACTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TATAAGCCTTCTACGCAAGACGTAGTTGCAGCATCAAAGAAGTCTTCGACTTGGGACTAT 1080

Qy   1081 TGGACTTCAGTAACCCCATTAAGTGGCCTCTGTATATGGAGTACAATTTTTCTTGTTATC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGGACTTCAGTAACCCCATTAAGTGGCCTCTGTATATGGAGTACAATTTTTCTTGTTATC 1140

Qy   1141 AGCCAGTTGGTTTTTTCAATACCATCCTTATAGTGTTTCAAGAAGGTTTGCTAACTTACCA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AGCCAGTTGGTTTTTTCAATACCATCCTTATAGTGTTTCAAGAAGGTTTGCTAACTTACCA 1200

Qy   1201 TATACTTTGTGGGTCATTACTTATAATTTACTATTTTTGACTGGGTACTGCTTGACTGAC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TATACTTTGTGGGTCATTACTTATAATTTACTATTTTTGACTGGGTACTGCTTGACTGAC 1260

Qy   1261 AAAATTTTCGGTAATTCTTCGGAATATTATAAAGTTGCCGAATGCTTGGAATCAATCAAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAAATTTTCGGTAATTCTTCGGAATATTATAAAGTTGCCGAATGCTTGGAATCAATCAAC 1320

Qy   1321 TCCAATGGGTTGTTTTTATTTTTGTTGGCAAATGTCTCTACTGGTTTAGTCAATATGTCT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TCCAATGGGTTGTTTTTATTTTTGTTGGCAAATGTCTCTACTGGTTTAGTCAATATGTCT 1380

Qy   1381 ATGGTCACGATAGATTCTTCACCCTTAAAATCATTCCTGGTTTTGTTGGCATACTGCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ATGGTCACGATAGATTCTTCACCCTTAAAATCATTCCTGGTTTTGTTGGCATACTGCTCA 1440

Qy   1441 TTCATAGCTGTCATATCGGTTTTCTTGTATAGAAAAAGAATATTCATTAAGCTATAA 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTCATAGCTGTCATATCGGTTTTCTTGTATAGAAAAAGAATATTCATTAAGCTATAA 1497
```